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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/419,901	10/18/1999	JENNIFER E. VAN EYK	1997-023-04U	2043

26259 7590 11/28/2001

LICATA & TYRRELL P.C.
66 E. MAIN STREET
MARLTON, NJ 08053

EXAMINER

COOK, LISA V

ART UNIT	PAPER NUMBER
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1641

DATE MAILED: 11/28/2001

13

Please find below and/or attached an Office communication concerning this application or proceeding.



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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
09/419,901	18 October 1999	Van Eyk et al.	1997-023-04U(PTQ-0028)

EXAMINER

Lisa V. Daniels-Cook

ART UNIT

PAPER

1641

13

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

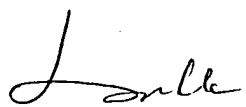
Commissioner of Patents

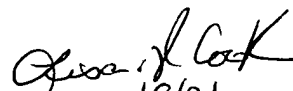
The communication filed 30 August 2001 is not fully responsive to the Office communication mailed 31 July 20001 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner **Lisa V. Daniels-Cook**, Art Unit 1641, whose telephone number is (703) 305-0808.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.


LONG V. LE
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600
11/19/01


11/8/01

Notice to Comply	Application No.		Applicant(s)	
	09/419,901		Van Eyk <i>et al.</i>	
	Examiner		Art Unit	
	Lisa V. Daniels-Cook		1641	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

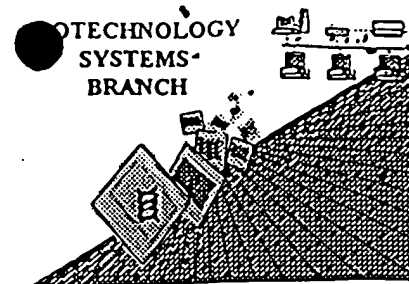
PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

L. Cook



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/419 901
Source: O I P E
Date Processed by STIC: 09.18.2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/419901

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE.

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/419,901

TIME: 16:19:44

Input Set : A:\Ptq-0021.app

Output Set: N:\CRF3\09182001\I419901.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Van Eyk, Jennifer E
 4 Labugger, Ralf
 5 Neverova, Irena
 7 <120> TITLE OF INVENTION: Methods of Diagnosing Muscle Damage
 9 <130> FILE REFERENCE: 1997-023-04U
 11 <140> CURRENT APPLICATION NUMBER: 09/419,901
 C--> 12 <141> CURRENT FILING DATE: 2001-08-30
 14 <160> NUMBER OF SEQ ID NOS: 7
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 12
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Rattus sp.
 23 <220> FEATURE:
 24 <221> NAME/KEY: UNSURE
 25 <222> LOCATION: (1)..(2)
 27 <220> FEATURE:
 28 <221> NAME/KEY: UNSURE
 29 <222> LOCATION: (7)
 30 <223> OTHER INFORMATION: P/A
 32 <400> SEQUENCE: 1
 W--> 33 Xaa Xaa Lys Lys Pro Glu Xaa Lys Ala Asp Asp Ala
 34 1 5 10
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 12
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Rattus sp.
 42 <220> FEATURE:
 43 <221> NAME/KEY: UNSURE
 44 <222> LOCATION: (1)
 46 <400> SEQUENCE: 2
 W--> 47 Xaa Pro Ala Pro Ala Ala Ala Pro Ala Ala Ala Pro
 48 1 5 10
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 11
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Rattus sp.
 56 <220> FEATURE:
 57 <221> NAME/KEY: UNSURE
 58 <222> LOCATION: (1)
 60 <220> FEATURE:
 61 <221> NAME/KEY: UNSURE
 62 <222> LOCATION: (8)
 64 <400> SEQUENCE: 3
 W--> 65 Xaa Lys Val Ala Leu Gly Ala Xaa Gly Gly Ile
 66 1 5 10
 69 <210> SEQ ID NO: 4

FYI: P or A is the preferred format.
 Xaa can only represent a single residue. MH

When 221 field response is "UNSURE", you must describe the possible amino acids or modified amino acids in field 223.

Errored

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/419,901

DATE: 09/18/2001

TIME: 16:19:44

Input Set : A:\Ptq-0021.app

Output Set: N:\CRF3\09182001\I419901.raw

70 <211> LENGTH: 13
71 <212> TYPE: PRT
72 <213> ORGANISM: Rattus sp.
74 <220> FEATURE:
75 <221> NAME/KEY: UNSURE
76 <222> LOCATION: (1)..(2)
78 <400> SEQUENCE: 4
W--> 79 Xaa Xaa Leu Lys Asp Ile Thr Arg Arg Leu Lys Ser Ile
80 1 5 10
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 10
85 <212> TYPE: PRT
86 <213> ORGANISM: Rattus sp.
88 <220> FEATURE:
89 <221> NAME/KEY: UNSURE
90 <222> LOCATION: (1)..(2)
92 <400> SEQUENCE: 5
W--> 93 Xaa Xaa Lys Leu Val Arg Pro Pro Val Gln
94 1 5 10
97 <210> SEQ ID NO: 6
98 <211> LENGTH: 10
99 <212> TYPE: PRT
100 <213> ORGANISM: Rattus sp.
102 <220> FEATURE:
103 <221> NAME/KEY: UNSURE
104 <222> LOCATION: (1)
106 <400> SEQUENCE: 6
W--> 107 Xaa Ala His Lys Ser Glu Ile Ala His Arg
108 1 5 10
111 <210> SEQ ID NO: 7
112 <211> LENGTH: 11
113 <212> TYPE: PRT
114 <213> ORGANISM: Rattus sp.
116 <220> FEATURE:
117 <221> NAME/KEY: UNSURE
118 <222> LOCATION: (1)
120 <220> FEATURE:
121 <221> NAME/KEY: UNSURE
122 <222> LOCATION: (4)
123 <223> OTHER INFORMATION: R/L
125 <400> SEQUENCE: 7
W--> 126 Xaa Pro Ser Xaa Lys Phe Phe Val Gly Gly Asn
127 1 5 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/419,901

DATE: 09/18/2001

TIME: 16:19:45

Input Set : A:\Ptq-0021.app

Output Set: N:\CRF3\09182001\I419901.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:79 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:93 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7